

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/661,984 B
Source: IFW16
Date Processed by STIC: 05/24/2006

ENTERED

RAW SEQUENCE LISTING

DATE: 05/24/2006

PATENT APPLICATION: US/10/661,984B

TIME: 10:23:20

Input Set : A:\13751-056001.TXT

Output Set: N:\CRF4\05242006\J661984B.raw

CPG-6)

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```

65 aga cac ttc tcg gcc cgc gcc ccc gcc gcc tgc acc ccc atc tgc tct      359
66 Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
67 45          50          55          60
69 tcc ccg cgg gtc cgc gcg gcg ctg ggg ggc cgg gca gcg cgc tcg      407
70 Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
71          65          70          75
73 ggc agc ggg ggc gcg ggg tgc cgc ctg cgc tcg cag ctg gtg ccg gtg      455
74 Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
75          80          85          90
77 cgc gcg ctc ggc ctg ggc cac cgc tcc gac gag ctg gtg cgt ttc cgc      503
78 Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
79          95          100          105
81 ttc tgc acc ggc tcc tgc ccg cgc gcg cgc tct cca cac gac ctc agc      551
82 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
83          110          115          120
85 ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga ccg ccc ccg ggc tcc      599
86 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
87 125          130          135          140
89 cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc tac gaa gcg gtc      647
90 Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
91          145          150          155
93 tcc ttc atg gac gtc aac agc acc tgg aga acc gtg gac cgc ctc tcc      695
94 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
95          160          165          170
97 gcc acc gcc tgc ggc tgc ctg ggc tgagggctcg ctccagggct ttgcagactg      749
98 Ala Thr Ala Cys Gly Cys Leu Gly
99          175          180
101 gacccttacc ggtggctctt cctgcctggg accctccgc agagtccac tagccagcgg      809
102 cctcagccag ggacgaaggc ctcaaagctg agaggccct gccggtgggt gatgga      865
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 200
106 <212> TYPE: PRT
107 <213> ORGANISM: Homo sapiens
109 <220> FEATURE:
110 <221> NAME/KEY: SIGNAL
111 <222> LOCATION: (1)...(20)
113 <400> SEQUENCE: 2
114 Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser
115 -20          -15          -10          -5
116 Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
117          1          5          10
118 Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
119          15          20          25
120 Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
121          30          35          40
122 Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
123 45          50          55          60
124 Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
125          65          70          75

```

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```

126 Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
127      80      85      90
128 Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
129      95      100      105
130 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
131      110      115      120
132 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
133 125      130      135      140
134 Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
135      145      150      155
136 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
137      160      165      170
138 Ala Thr Ala Cys Gly Cys Leu Gly
139      175      180

```

141 <210> SEQ ID NO: 3

142 <211> LENGTH: 861

143 <212> TYPE: DNA

144 <213> ORGANISM: Homo sapiens

146 <220> FEATURE:

147 <221> NAME/KEY: CDS

148 <222> LOCATION: (7)...(717)

150 <221> NAME/KEY: 5'UTR

151 <222> LOCATION: (1)...(6)

W--> 153 <221> 3'UTR

154 <222> LOCATION: (718)...(861)

W--> 156 <221> sig_peptide

157 <222> LOCATION: (7)...(174)

W--> 159 <221> mat_peptide

160 <222> LOCATION: (298)...(717)

W--> 162 <221> mat_peptide

163 <222> LOCATION: (370)...(717)

W--> 165 <221> mat_peptide

166 <222> LOCATION: (379)...(717)

W--> 168 <400> 3

```

169 gagccc atg ccc ggc ctg atc tca gcc cga gga cag ccc ctc ctt gag      48
170      Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu
171      -55      -50      -45
173 gtc ctt cct ccc caa gcc cac ctg ggt gcc ctc ttt ctc cct gag gct      96
174 Val Leu Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala
175      -40      -35      -30
177 cca ctt ggt ctc tcc gcg cag cct gcc ctg tgg ccc acc ctg gcc gct      144
178 Pro Leu Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala
179      -25      -20      -15
181 ctg gct ctg ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc      192
182 Leu Ala Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro
183 -10      -5      1      5
185 cgc agc cct gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc      240
186 Arg Ser Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro
187      10      15      20

```

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```

189 gcc ggc cac ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga      288
190 Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg
191      25      30      35
193 gcc ccg cgg ccg ccg ccg cag cct tct ccg ccc gcg ccc ccg ccg cct      336
194 Ala Arg Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro
195      40      45      50
197 gca ccc cca tct gct ctt ccc cgc ggg ggc cgc gcg gcg ccg gct ggg      384
198 Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly
199 55      60      65      70
201 ggc ccg ggc aac cgc gct ccg gca gcg ggg gcg ccg ggc tgc cgc ctg      432
202 Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu
203      75      80      85
205 cgc tcg cag ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc      480
206 Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser
207      90      95      100
209 gac gag ctg gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg      528
210 Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala
211      105      110      115
213 cgc tct cca cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc      576
214 Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Gly Ala Gly Ala
215      120      125      130
217 ctg cga ccg ccc ccg ggc tcc ccg ccc gtc agc cag ccc tgc tgc cga      624
218 Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg
219 135      140      145      150
221 ccc acg cgc tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg      672
222 Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp
223      155      160      165
225 aga acc gtg gac cgc ctc tcc gcc aac ccc tgc ggc tgc ctg ggc      717
226 Arg Thr Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly
227      170      175      180
229 tgagggctcg ctccagggct ttgcagactg gacccttacc ggtggctctt cctgcctggg      777
230 accctccgc agatccac tagccagcgg cctcagccag ggacgaaggc ctcaaagctg      837
231 agaggccct gccggtgggt gatg      861
233 <210> SEQ ID NO: 4
234 <211> LENGTH: 237
235 <212> TYPE: PRT
236 <213> ORGANISM: Homo sapiens
238 <220> FEATURE:
239 <221> NAME/KEY: SIGNAL
240 <222> LOCATION: (1)...(56)
242 <400> SEQUENCE: 4
243 Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu Val Leu
244 -55 -50 -45
245 Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala Pro Leu
246 -40 -35 -30 -25
247 Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala
248 -20 -15 -10
249 Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser
250 -5 1 5

```

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```

251 Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly
252      10      15      20
253 His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg
254 25      30      35      40
255 Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Ala Pro
256      45      50      55
257 Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro
258      60      65      70
259 Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser
260      75      80      85
261 Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu
262      90      95      100
263 Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser
264 105      110      115      120
265 Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg
266      125      130      135
267 Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr
268      140      145      150
269 Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr
270      155      160      165
271 Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly
272      170      175      180

```

274 <210> SEQ ID NO: 5

275 <211> LENGTH: 140

276 <212> TYPE: PRT

277 <213> ORGANISM: Homo sapiens

279 <220> FEATURE:

280 <221> NAME/KEY: VARIANT

281 <222> LOCATION: 134

282 <223> OTHER INFORMATION: Xaa = Asn or Thr

284 <221> NAME/KEY: VARIANT

285 <222> LOCATION: 135

286 <223> OTHER INFORMATION: Xaa = Ala or Pro

W--> 288 <400> 5

```

289 Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro
290 1      5      10      15
291 Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
292      20      25      30
293 Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
294      35      40      45
295 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
296      50      55      60
297 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
298 65      70      75      80
299 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
300      85      90      95
301 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
302      100      105      110
303 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\13751-056001.TXT
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 134,135

Seq#:6; Xaa Pos. 110,111

Seq#:7; Xaa Pos. 107,108

Seq#:27; N Pos. 1

Seq#:76; Xaa Pos. 5,6,7,8,9,10,11,12,15,21,22,23,24,25,26,27,28,29,30,31,32

Seq#:76; Xaa Pos. 33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51

Seq#:76; Xaa Pos. 53,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75

Seq#:76; Xaa Pos. 76,77,78,79,82,83

VERIFICATION SUMMARY

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Input Set : A:\13751-056001.TXT

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L:37 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:40 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:43 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:153 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:156 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:159 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:162 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:165 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:168 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:288 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:128
L:322 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:96
L:354 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:96
L:384 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:387 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:390 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:393 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:396 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:399 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:477 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:861 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:865 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:27
L:866 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:1749 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1753 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:76
L:1757 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:76
L:1758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0
M:341 Repeated in SeqNo=76